STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/510,698*

PCT/10

Source:

Date Processed by STIC: *7/5/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/510,698

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

·2 ____ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ **Misaligned Amino** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering use space characters, instead.

4 ____ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ____ **Variable Length** Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ **PatentIn 2.0** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 ____ **Skipped Sequences** Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) . SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ **Skipped Sequences** Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000

9 ____ **Use of n's or Xaa's** Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ **Invalid <213>** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ____ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ **PatentIn 2.0** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 07/05/2005
PATENT APPLICATION: US/10/510,698   TIME: 11:16:36

Input Set : **A:\MHKBERLIN.ST25.txt**
Output Set: **N:\CRF4\07052005\J510698.raw**

```
 3 <110> APPLICANT: EPIGENOMICS AG
 4        BERLIN, KURT
 6 <120> TITLE OF INVENTION: METHOD FOR ANALYSIS OF METHYLATED NUCLEIC ACIDS
 8 <130> FILE REFERENCE: MHK-051-004
10 <140> CURRENT APPLICATION NUMBER: US 10/510,698
11 <141> CURRENT FILING DATE: 2004-10-08
13 <150> PRIOR APPLICATION NUMBER: PCT/IB03/01791
14 <151> PRIOR FILING DATE: 2003-04-09
16 <150> PRIOR APPLICATION NUMBER: US 60/370,690
17 <151> PRIOR FILING DATE: 2002-04-09
19 <160> NUMBER OF SEQ ID NOS: 15
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 22
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial
28 <220> FEATURE:
29 <223> OTHER INFORMATION: oligonucleotide primer
31 <400> SEQUENCE: 1
32 ttttcgtcgt tttaggttat cg                                         22
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 23
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial
40 <220> FEATURE:
41 <223> OTHER INFORMATION: oligonucleotide primer
43 <400> SEQUENCE: 2
44 tttttgttgt tttaggttat tgg                                        23
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 26
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial
52 <220> FEATURE:
53 <223> OTHER INFORMATION: oligonucleotide probe
55 <400> SEQUENCE: 3
56 ttcggacgtc gttgttcggt cgatgt                                     26
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 23
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial
64 <220> FEATURE:
65 <223> OTHER INFORMATION: oligonucleotide primer
67 <400> SEQUENCE: 4
```

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```
 68 tttttgttgt tttaggttat tgg                                        23
 71 <210> SEQ ID NO: 5
 72. <211> LENGTH: 21
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Artificial
.76 <220> FEATURE:
 77 <223> OTHER INFORMATION: oligonucleotide primer
 79 <400> SEQUENCE: 5
 80 catatgctgt gaataaatta c                                          21
 83 <210> SEQ ID NO: 6
 84 <211> LENGTH: 26
 85 <212> TYPE: DNA
 86 <213> ORGANISM: Artificial
 88 <220> FEATURE:
 89 <223> OTHER INFORMATION: oligonucleotide probe
 91 <400> SEQUENCE: 6
 92 tttggatgtt gttgtttggt tgatgt                                     26
 95 <210> SEQ ID NO: 7
 96 <211> LENGTH: 17
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Artificial
100 <220> FEATURE:
101 <223> OTHER INFORMATION: oligonucleotide primer
103 <400> SEQUENCE: 7
104 cggatacgat ttcgggg                                               17
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 22
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial
112 <220> FEATURE:
113 <223> OTHER INFORMATION: oligonucleotide primer
115 <400> SEQUENCE: 8
116 atacgataaa cgcaacaacg ac                                         22
119 <210> SEQ ID NO: 9
120 <211> LENGTH: 29
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial
124 <220> FEATURE:
125 <223> OTHER INFORMATION: oligonucleotide probe
127 <400> SEQUENCE: 9
128 atttggagtt tcgtgattcg cgttacgga                                  29
131 <210> SEQ ID NO: 10
132 <211> LENGTH: 19
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial
136 <220> FEATURE:
137 <223> OTHER INFORMATION: oligonucleotide primer
139 <400> SEQUENCE: 10
140 tggatatgat tttggggta                                             19
```

```
143 <210> SEQ ID NO: 11
144 <211> LENGTH: 24
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial
148 <220> FEATURE:
149 <223> OTHER INFORMATION: oligonucleotide primer
151 <400> SEQUENCE: 11
152 atatgataaa tgcaacaatg acat                                24
155 <210> SEQ ID NO: 12
156 <211> LENGTH: 29
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial
160 <220> FEATURE:
161 <223> OTHER INFORMATION: oligonucleotide probe
163 <400> SEQUENCE: 12
164 atttggagtt ttgtgatttg tgttatgga                           29
167 <210> SEQ ID NO: 13
168 <211> LENGTH: 25
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial
172 <220> FEATURE:
173 <223> OTHER INFORMATION: oligonucleotide primer
175 <400> SEQUENCE: 13
176 tccatattcc aaaccctata ccaaa                               25
179 <210> SEQ ID NO: 14
180 <211> LENGTH: 22
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial
184 <220> FEATURE:
185 <223> OTHER INFORMATION: oligonucleotide primer
187 <400> SEQUENCE: 14
188 tgggattgag ggtaagaggg at                                  22
191 <210> SEQ ID NO: 15
192 <211> LENGTH: 22
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial
196 <220> FEATURE:
197 <223> OTHER INFORMATION: artificial sequence
199 <400> SEQUENCE: 15
200 attagtttcg tttaaggttc ga                                  22
```

insufficient explanation - what is source?
(see item 11 on Error summary sheet)

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<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15

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